

Index

A

- AAA+ proteins, 78, 79, 81, 83, 86, 87, 238
- Aging, 4, 13, 18, 55, 123–140, 220
- Agonists of HR and HDR, 55, 56, 64, 126, 131, 137, 162, 167, 171–174, 185–198, 214, 248, 249, 252, 257, 288
- Anchoring module, 250, 253–254
- Antagonists of HR and HDR, 55, 56, 64, 126, 131, 137, 162, 167, 171–174, 185–198, 214, 248, 249, 252, 257, 288
- ASCE P loop ATPases, 78
- ATPase, 20, 24, 25, 31, 48, 59, 60, 78, 79, 83, 86–88, 104, 125, 128, 131–136, 155, 169, 194, 195, 211–215, 217, 226, 227, 229–234, 236–238, 246, 251, 252, 255, 267, 268, 270–274, 276, 277, 280–283, 285, 286, 289
- ATP-dependent chromatin remodeling, 18, 263–289

B

- Base excision repair (BER), 203–220
- BLM. *See* Bloom syndrome protein (BLM)
- BLM helicase, 56, 62, 126, 132, 133, 137, 168, 190–191
- Bloom syndrome, 13, 18, 55, 56, 126, 132, 162, 190–191
- Bloom syndrome protein (BLM), 3, 19, 53, 123, 161, 185, 218
- Brownian ratchet, 7–8

C

- Cancer, 4, 13, 18, 55, 123–140, 162, 179, 186, 190, 191, 193, 218, 220
- Cell proliferation, 248–250
- Cellular functions, 128, 135, 247–250, 270, 284
- CHD. *See* Chromodomain, Helicase, DNA binding (CHD)
- Chromatin, 3, 18, 48, 124, 233, 263
- Chromodomain, Helicase, DNA binding (CHD), 60, 61, 267, 268, 270, 276, 289
- Conjugation, 246–249
- Coordinated escort, 89, 90

D

- Damage recognition, 136, 204–206, 211–213, 218, 219, 238
- Damage verification, 204, 205, 207–209, 212–216
- Dimer, 32, 61, 66, 167, 216, 217, 237, 238, 246, 248, 249, 251, 252, 254, 257, 264–266, 269, 270, 276, 277, 281, 283–284

DNA

- helicases, 3–6, 9–13, 17–35, 47–68, 77, 101, 123–140, 185–198, 203–220, 246, 251, 267, 268, 273, 278
- polymerase, 34, 55, 97, 99, 103–104, 106–109, 146, 153, 194, 197, 211, 217–220
- pumps, 245–258
- repair, 4, 18, 19, 58, 61, 67, 76, 79, 113, 124, 127–129, 131, 135–139, 162, 188, 189, 196, 204, 209, 212, 214, 216, 220, 267, 270, 277, 285, 288, 289

- DNA (*cont.*)
 replication, 3, 4, 13, 18, 53, 60, 76, 79, 82, 97, 98, 101, 124, 126, 127, 135, 150, 165, 174–177, 193, 194, 197, 249, 267, 270, 288
 substrate requirements, 167–169
 DnaB, 7, 33, 80, 81, 83, 85, 91, 98, 99, 101, 103–106, 111–113
 DnaB helicase, 81, 91, 98, 99, 106, 111
 DNA double-strand break repair (DSBR) pathways, 186, 214
- E**
 Effective herpesvirus antivirals, 145–157
 E1 helicase, 79, 81, 83, 85, 89, 90
 Endonuclease, 54, 107, 109, 174, 189, 193, 194, 208, 215, 219, 220, 232, 234
- F**
 Features of RecQ helicases, 162–165
 FtsK family, 245–258
 Function, 1, 18, 48, 75, 97, 124, 146, 162, 185, 226, 263
 Functionally important binding partners, 166–167
- G**
 Genome maintenance, 54, 57, 60, 110, 186, 190, 225
 Genomic integrity, 2, 161–179
 stability, 3, 55, 125–127, 134, 204
 GTPase, 86, 226–228
 Guardians of genomic integrity, 161–179
- H**
 Helicase(s), 1–14, 17–35, 47–68, 75–92, 97–113, 123–140, 145–157, 161–179, 185–198, 203–220, 225–238, 246, 251, 252, 267, 268, 270–271, 273, 278
 Helicase-primase complex, 145–157
 Helicase-primase inhibitors, 145, 152
 Herpesvirus chemotherapy, 145–147
 Histone
 chaperone, 263, 266, 283, 284, 288
 post-translational modifications (PTMs), 82, 263
 variant, 266, 286–288
- Homologous repair pathways, 186–187
 Human genetic disease, 14, 124, 126
- I**
 Improved inhibitors, 147
 INO80, 60–63, 267, 268, 270, 277, 283, 288, 289
 ISWI, 60, 61, 267, 268, 270–284, 286–289
- M**
 MCM. *See* Minichromosome maintenance (MCM)
 MCM helicase, 79, 82, 85
 Mechanisms, 1, 18, 48, 75, 97, 124, 162, 226, 263
 Mediation of homologous recombination, 185–198
 Minichromosome maintenance (MCM), 79, 81, 82–85, 100, 102, 104
 Mismatch repair (MMR), 190, 203–220, 237
 MMR. *See* Mismatch repair (MMR)
 Motor, 3, 17, 75, 113, 124, 162, 204, 225, 246, 268
 Mutation, 18, 24, 29, 127–135, 154–156, 164, 165, 169, 186, 190, 194–196, 251
- N**
 NER. *See* Nucleotide excision repair (NER)
 Nucleosome, 3, 4, 13, 60, 61, 64, 66, 67, 264–289
 Nucleotide excision repair (NER), 57, 58, 107, 125, 128, 135, 136, 138, 204–217, 238
- O**
 Octamer, 3, 60, 66, 264, 265, 268, 269, 271, 272, 275–284, 289
 Okazaki fragments, 34, 107–109, 189, 195
 Orientation module, 250, 252–253
 Overview, 1–13, 80–83, 125, 139, 172, 204
- P**
 Powerstroke, 7–8
 Primase, 18, 81, 99, 104–105, 112, 148, 154–157
 Prospects for HP inhibitors (HPI), 157
- Q**
 Quaternary structure, 83–85, 98

R

RecA fold, 78–80, 90, 226–228, 230, 232
 Recombination, 3, 13, 14, 18, 34, 53, 55, 56, 58–60, 62, 64, 79, 111–113, 124, 126, 131, 137, 162, 165, 167, 171–174, 177, 179, 185–198, 204, 214, 216, 248, 249, 251–253, 257, 267, 288
 RecQ helicases, 55, 56, 62–63, 110, 126, 127, 132, 133, 161–179, 185, 188–190, 218
 Regulation of homologous recombination, 185–198
 Replication, 3, 18, 48, 76, 97, 124, 146, 161, 204, 236, 249, 267
 Replication repair, 52, 60, 177
 Rho helicase, 77, 80, 85, 8991

S

Sequential mechanism, 87, 88, 91
 SF1 helicases, 8, 9, 18, 22, 23, 25, 28–32, 34, 48, 198, 204, 205
 Single-molecule, 6, 11, 13, 14, 29, 31–32, 57, 62–65, 91, 233, 234, 236, 239, 254, 266, 274, 275, 277, 280, 283, 284, 288, 289
 Sliding, 28, 103, 235–237, 269–272, 275, 276, 278, 280
 Sporulation, 246, 247, 249, 254

Structure, 1, 17, 47, 75, 98, 124, 149, 164, 185, 206, 226, 245, 264
 Superfamilies SF3-SF6, 75, 76, 79, 80, 84
 Superfamily, 28, 48, 50, 80–83, 162, 185, 193, 226, 237, 250, 254, 267
 Superfamily II (SF2), 5, 8, 9, 22, 26–29, 47–68, 76, 77, 125, 126, 162, 185, 193, 204–206, 209, 213, 226, 229, 232, 238, 267, 268, 271, 278
 SWI/SNF, 3, 48, 52, 61–62, 66–68, 267, 268, 270, 272–276, 278–281, 283, 284, 288, 289
 Switch, 5, 7, 31, 34, 61, 66, 68, 80, 87, 112, 212, 225–239

T

Tetramer, 102, 264–266, 288
 T7 helicase, 12, 81, 83, 88, 90, 91
 Translocases, 5–8, 14, 20, 32, 35, 48–50, 53–55, 59, 60, 64, 68, 76, 77, 82, 130, 131, 164, 193, 217, 226, 229, 233–235, 238, 246, 251, 253, 272–274, 278, 280
 Translocation, 5, 19, 48, 80, 99, 125, 186, 209, 228, 245, 268

U

Unwinding, 6, 18, 52, 75, 98, 124, 164, 189, 204, 225